

# Estimation of methane and its variation across different breeds of cattle predicted from milk fatty acids

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<sup>2</sup> ITN-Marie Curie GreenHouseMilk Project

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GreenHouseMilk mid term review, December 2011 –Paris – France



# Timeline

Undergraduate- Veterinary Science -2001- Tribhuvan University

MSc Animal Science -specialization Animal Breeding and Genetics

Wageningen University, the Netherlands

## Molecular Characterization of a QTL associated with Pulmonary Hypertension Syndrome in Chicken

Purna Kandel ABG80436

Supervisors:

Ir. Martin Elferink

Dr. Richard Crooijmans

Animal Breeding & Genomics Centre



## Linkage Disequilibrium for chromosome 6 of Dutch Holstein Friesians

Purna Bhadra Kandel

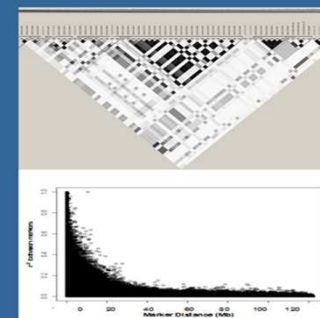
ABG 80424

12<sup>th</sup> Aug 2010

Supervisors:

Dr. Marleen Visker

Dr. Henk Bovenhuis



WAGENINGEN UNIVERSITY  
ANIMAL SCIENCES

Animal Breeding &  
Genomics Centre

Worked as Livestock Development Officer for Department of Livestock Services, Nepal 2003-2008 and 2010-2011

# Expectation from Group- GreenHouseMilk Project

- Scientific course on computer programming
- Soft skills training –Writing scientific papers
- Observation of different livestock (dairy) production system in partner countries



## Elucidate the relationships that may exist between milk fatty acids and environmental impact traits

- **37% of anthropogenic methane emission from Livestock**
- **Methane is the largest contributor to total GHG emissions from the dairy sector - accounting for over half of total emissions**  
(FAO, 2006; 2010)

# Methane Prediction through milk FA composition

- The fermentation of feed in rumen is essentially a digestion process of ruminants and methane is produced
- Large number of FA are synthesized, degraded in rumen in this process
- These FA are absorbed in blood; some are secreted directly to milk and others *de novo* synthesis in mammary gland
- Therefore; there should be link between milk fatty acids and CH<sub>4</sub> production → prediction equation

(Chilliard et al., 2000 & 2009; Moss et al., 2000; Dijkstra et al., 2011 )

# Methane Prediction Equations

Prediction	Equation	R <sup>2</sup>	Reference
Methane1 g/day	$9.97 \times (\text{C8:0 to C16:0}) - 80$	0.88	Chilliard et al., 2009
Methane2 g/day	$-8.72 \times \text{C18:0} + 729$	0.88	Chilliard et al., 2009
Methane3 g/day	$282 \times \text{C8:0} + 11$	0.81	Chilliard et al., 2009
Methane4 g/day	$16.8 \times \text{C16:0} - 77$	0.82	Chilliard et al., 2009
Methane5 g/kg DM, 17.7 kg DM/day	$24.6 + 8.74 \times \text{C17:0 anteiso} - 1.97$ $\times \text{trans-10+11 C18 :1} - 9.09 \times$ $\text{C18 :1 cis-11} + 5.07 \times \text{C18 :1 cis-13}$	0.73	Dijkstra et al., 2011

# MIR Prediction of CH<sub>4</sub>

- Milk fatty acids can be predicted by Mid-Infrared (MIR) spectrometry (FP7 RobustMilk)
  - Soyeurt et al., Journal of Dairy Science 2011
- Development of MIR equations to predict CH<sub>4</sub> based on equations published in the literature
  - Calibration dataset used in the RobustMilk project
    - Gas chromatographic data from Ireland, Scotland and Walloon Region of Belgium



# MIR Prediction of CH<sub>4</sub> Indicators

Prediction equations for CH<sub>4</sub> based on Walloon data

Indicator	N	Mean	SD	R <sup>2</sup> cv
Methane1	597	446.75	68.50	0.92
Methane2	602	421.52	60.71	0.91
Methane3	595	368.53	43.23	0.72
Methane4	588	459.55	88.11	0.92
Methane5	592	20.81	2.90	0.69

R<sup>2</sup>cv = cross-validation coefficient of determination

The same work will be done in the next weeks based on all available RobustMilk data



# The principal components

- Tristant et al., (submitted) categorized milk FA through PCA into two principal component
- (17340 test day solutions from initial records of 209,709 Holstein first lactation cow)
  - The **PC1**: related to Methanogenesis and –ve of it is Environmental friendly
  - The **PC2**: constitutes polyunsaturated FA owing to better nutrition to human health
  - The **mpc**: mean of PC1 and PC2 (equal weightage given to both PCs)
  - **mpc16ALA**: Linear combination of C16 with ALA; indicator similar characteristics to the mpc (Pierre Weill-personal communication)

Proportion	PC1	PC2
	0.52	0.21
Eigenvectors		
C4	0.21	0.26
C6	0.32	0.13
C8	0.33	0.06
C10	0.32	-0.04
C12	0.32	-0.07
C14	0.35	-0.03
C14_1c	0.32	-0.12
C16	0.33	0.00
C16_1c	0.27	0.08
C17	0.27	0.25
C18	-0.07	0.49
C18_1c9	-0.04	0.48
C18_2c9c12	0.09	0.23
C18_3c9c12c15	-0.06	0.45
C18_2c9t11	-0.21	0.31

# Objectives of this first work

1. Study of the variation of these 8 methane indicator traits and PC2 predicted by MIR across **breeds, DIM and lactation number**
2. Estimation of **genetic parameters** for Dual Purpose Belgian Blue cattle
  - heritability and genetic correlations
3. Appreciation of the genetic variability (**EBV**) for the Dual Purpose Belgian Blue cattle

# Originality

- MIR predictions of methane indicator traits
  - Easy to implement in practice
  - Do not use ratio → big bias
  - Low cost
- Large MIR dataset: more than 1,800,000 records collected partly through the RobustMilk project



# Original Dataset

Breed	Records	Milk (kg/day)		Fat percent (g/dl of milk)		Protein percent (g/dl of milk)	
		Mean	SD	Mean	SD	Mean	SD
DP Belgian Blue	16,825	15.21	6.01	3.64	0.52	3.42	0.37
Holstein	963,624	25.19	8.57	4.15	0.64	3.49	0.64
Jersey	778	13.99	4.39	4.88	0.71	3.92	0.42
Red and White	1,162	17.50	7.33	4.39	0.63	3.75	0.48
Normande	14,856	22.11	7.32	4.03	0.58	3.60	0.37
Montbeliarde	4,263	19.11	6.67	4.36	0.63	3.70	0.40

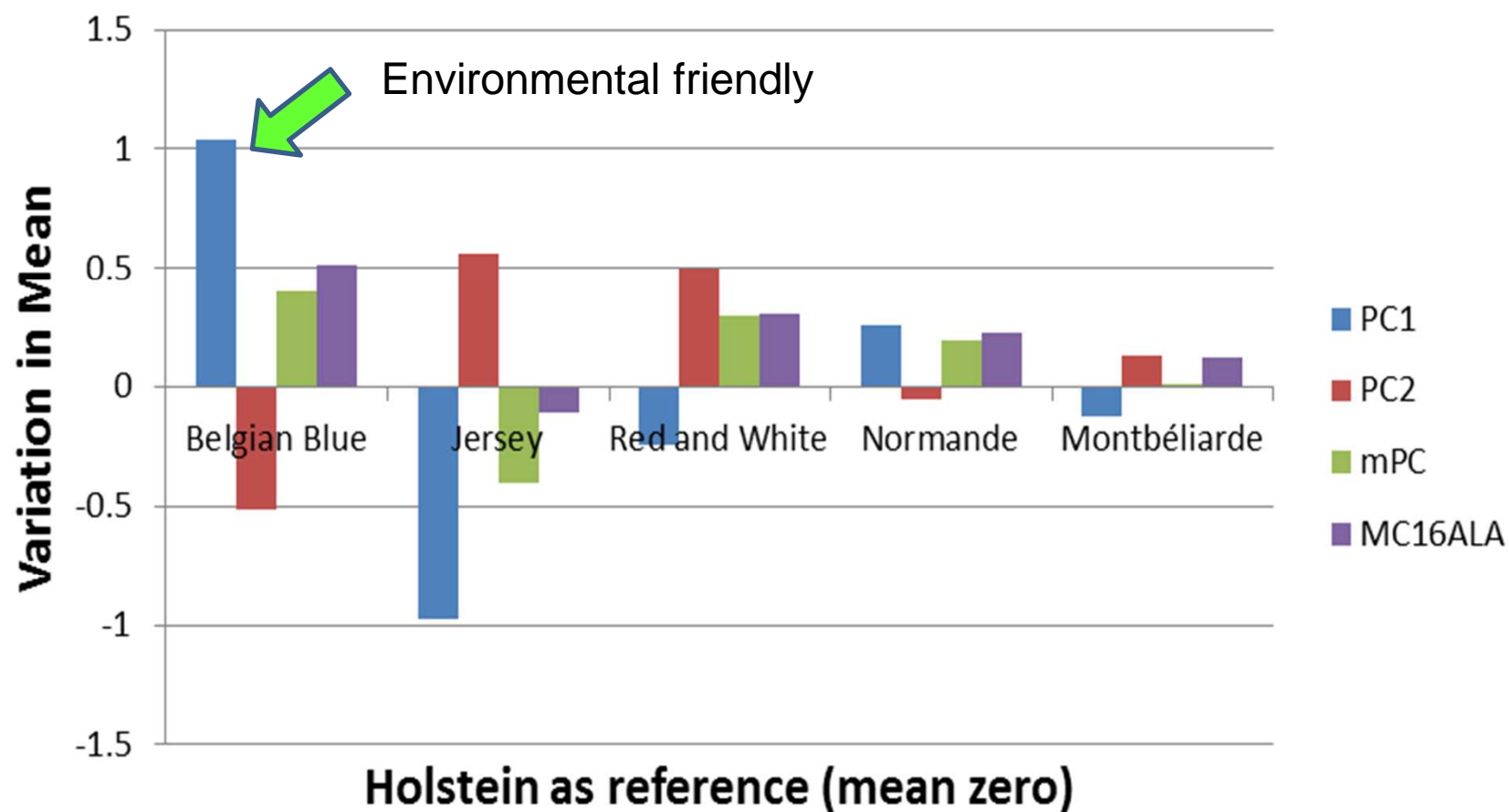
MIR spectral were collected from the Walloon Region of Belgium between Jan. 2007 to Oct. 2011

- Correction for outliers (data with mean  $\pm 3 \times \text{SD}$  were deleted)

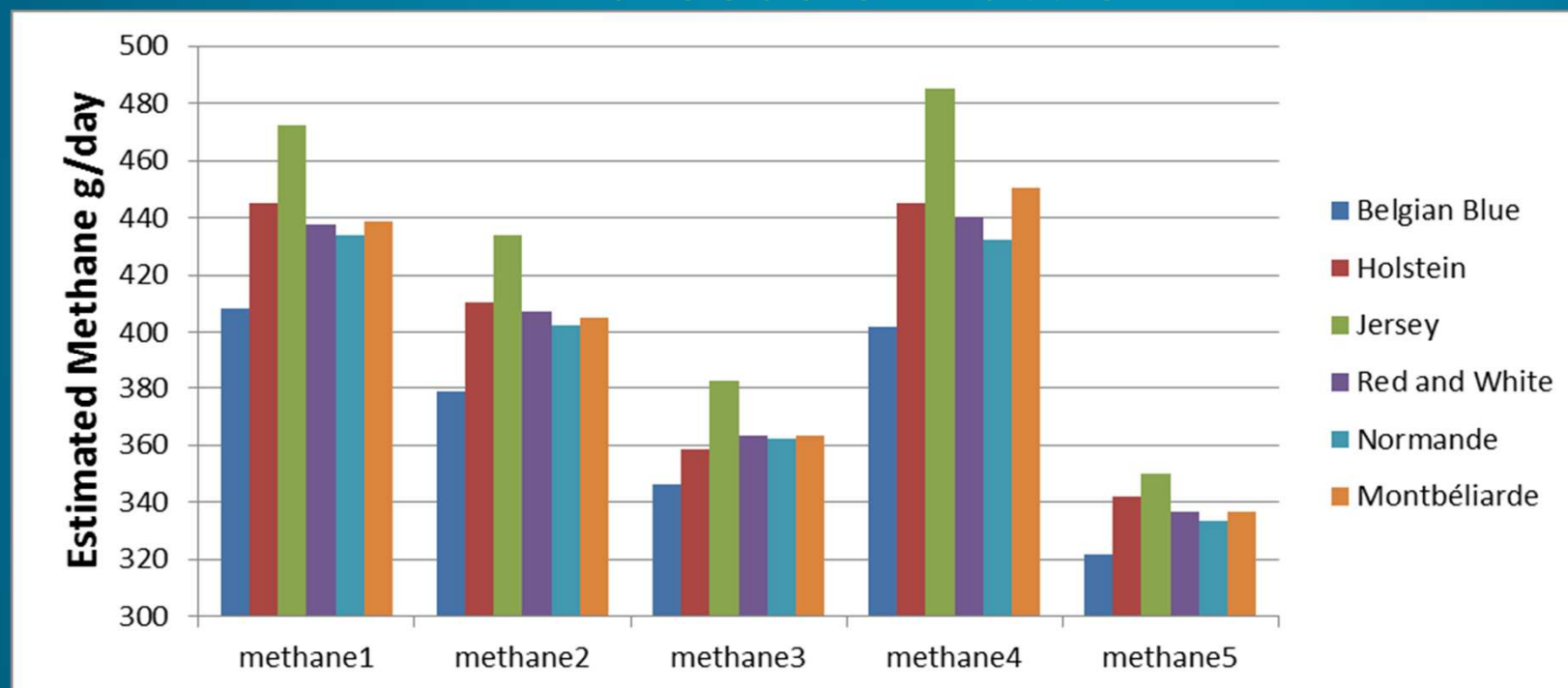
# Observed correlations

	PC1	PC2	mPC	mpc16ALA	methane1	methane2	methane3	methane4	methane5
PC1	1								
PC2	-0.59	1							
mPC	0.45	0.45	1						
mpc16ALA	0.47	0.32	0.87	1					
methane1	-0.65	0.01	-0.69	-0.59	1				
methane2	-0.64	0.03	-0.68	-0.58	0.99	1			
methane3	-0.43	0.09	-0.37	-0.19	0.51	0.52	1		
methane4	-0.55	-0.03	-0.63	-0.65	0.88	0.88	0.25	1	
methane5	-0.42	-0.04	-0.51	-0.52	0.61	0.65	0.16	0.65	1

# Comparison of PC1, PC2, mpc and mc16ALA across breeds



## Estimated methane production by different breeds of Cattle

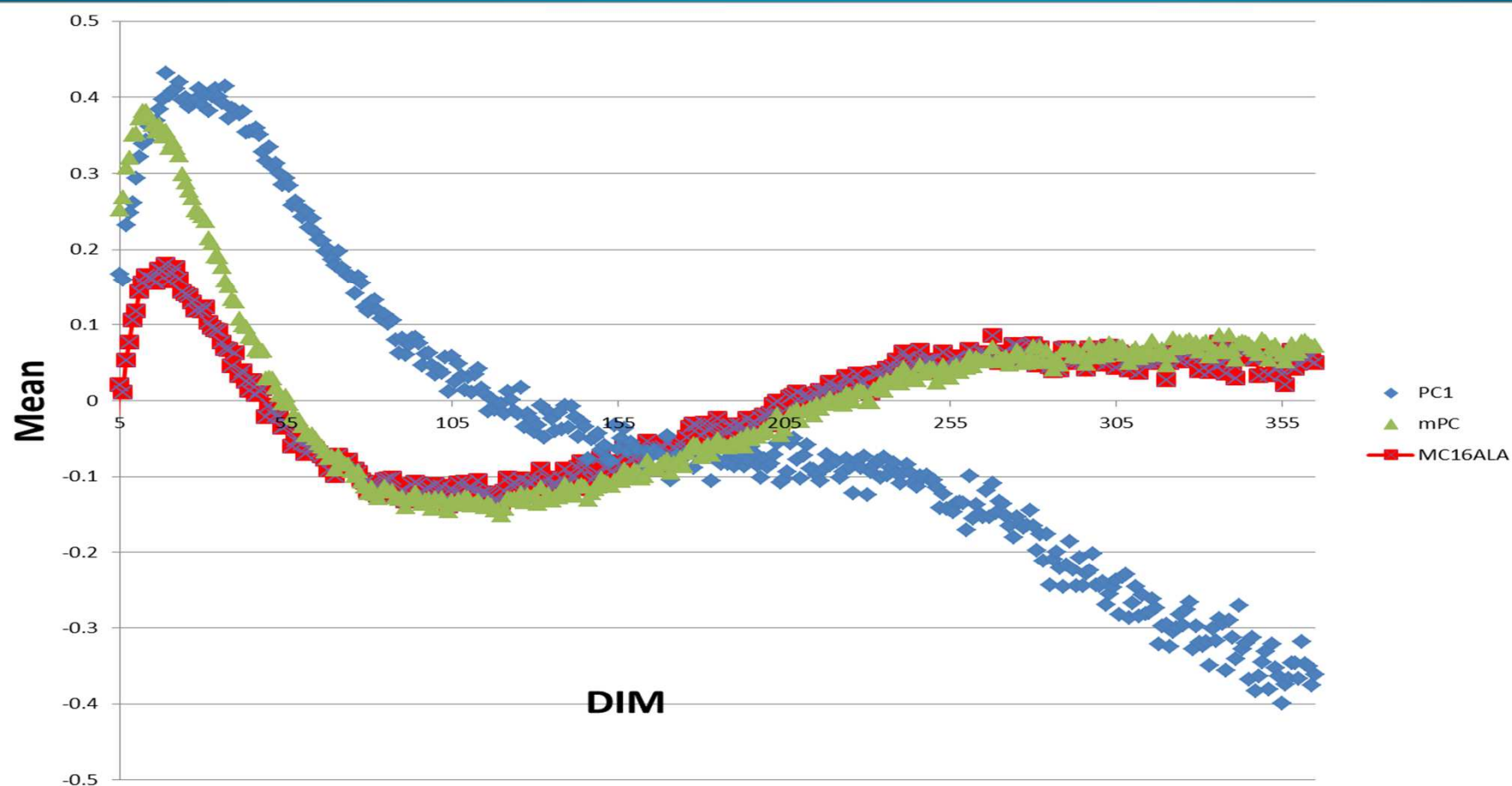


Methane Emissions	Holstein	Jersey	Hol × Jersey F1
g/day	403	356	415
g/kg milk solids	282	274	274

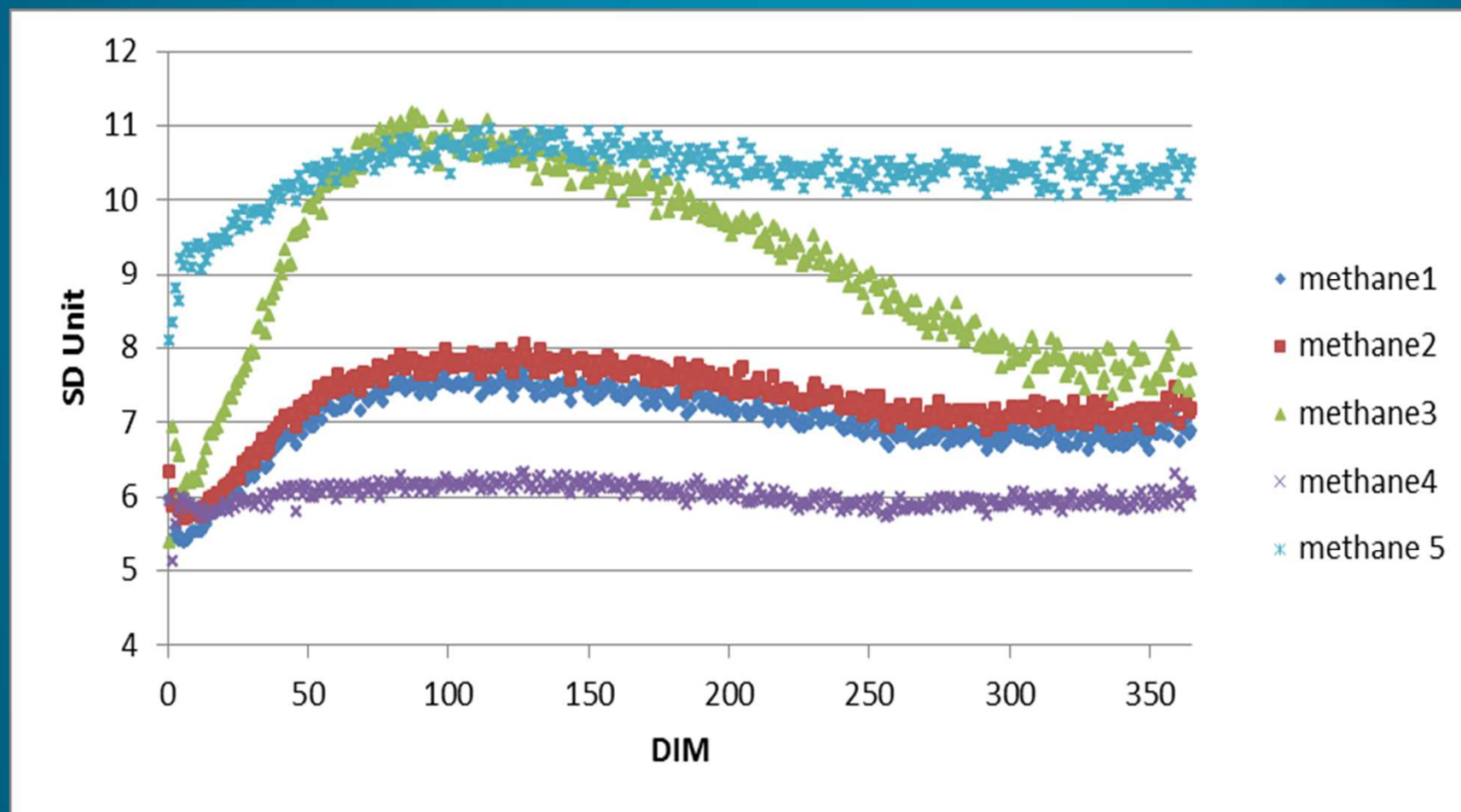
SF6 technique (Deighton et. al.2011)



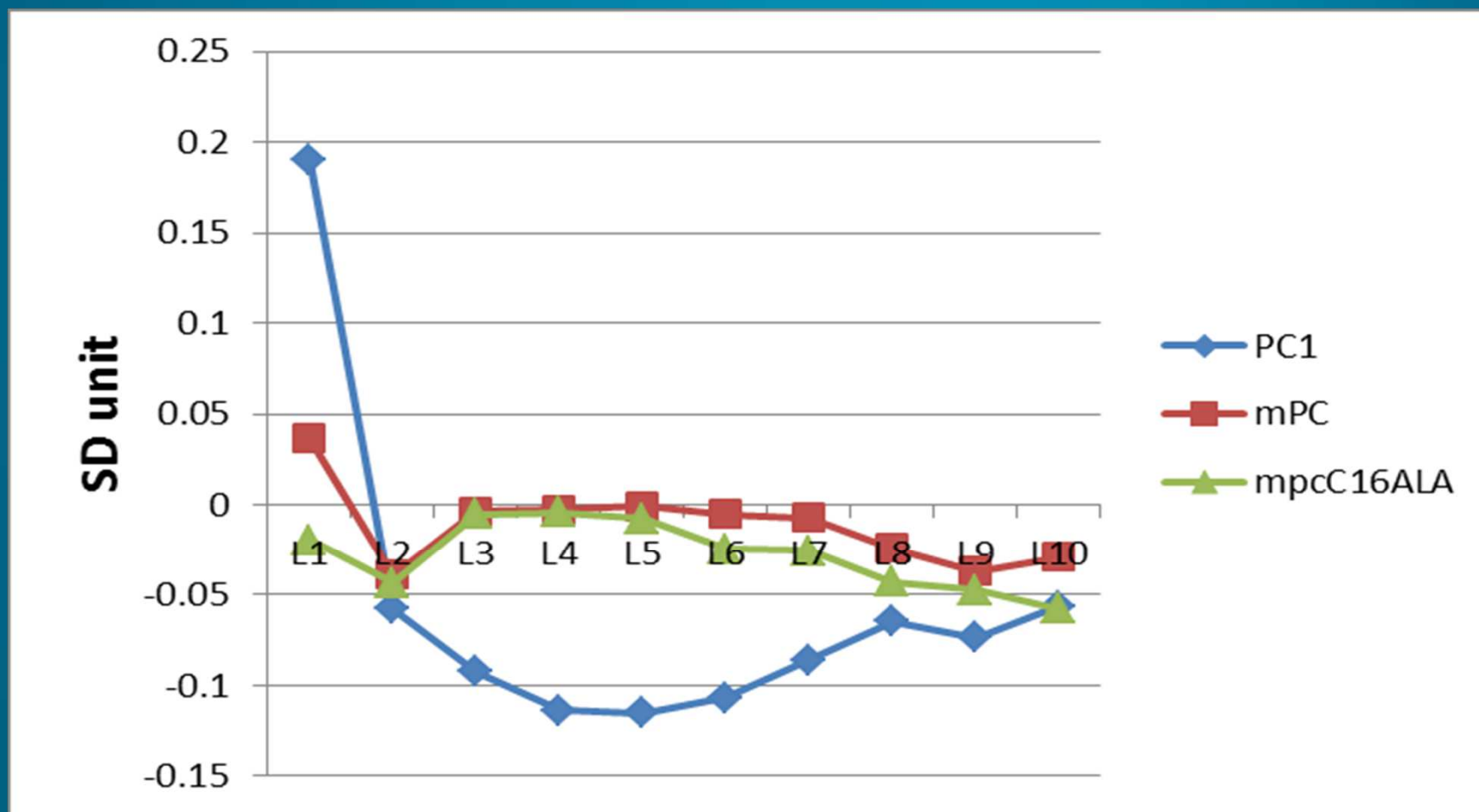
# Change in PCs with respect to DIM



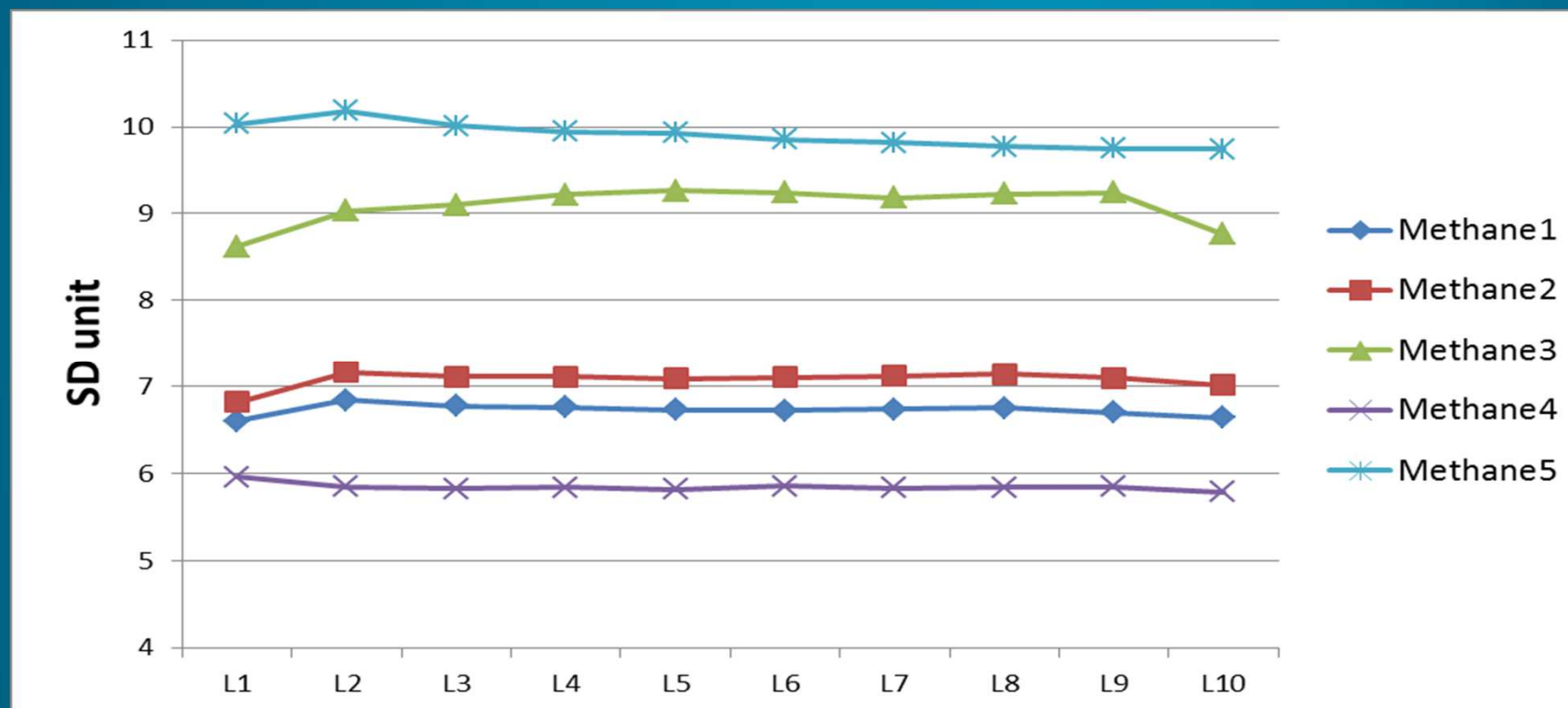
# Predicted Methane on DIM



# PCs on Lactation Numbers



# Methane prediction on lactation numbers



- It has important implication; we can predict lifetime methane emission only from few lactations

# Genetic Parameters for Dual Purpose Belgian Blue





# Single trait test-day model

	Records	Milk (kg/day)		Fat percent (g/dl of milk)		Protein percent (g/dl of milk)	
		Mean	SD	Mean	SD	Mean	SD
All Lactation	16,825	15.21	6.01	3.64	0.52	3.42	0.37
Lactation 1	5,622	13.02	4.20	3.67	0.49	3.45	0.35
Lactation 2	3,851	15.28	5.64	3.66	0.51	3.44	0.36
Lactation 3	2,526	16.74	6.29	3.62	0.51	3.41	0.37

$$y = X\beta + Q(Zp + Zu) + e$$

$y$ : separate 9 traits

$\beta$ : fixed effects - HTD, DIM (24 classes) and age at calving (3 classes)

$p$ : random permanent environmental effects

$u$ : additive genetic effects

$e$ : random residual effect

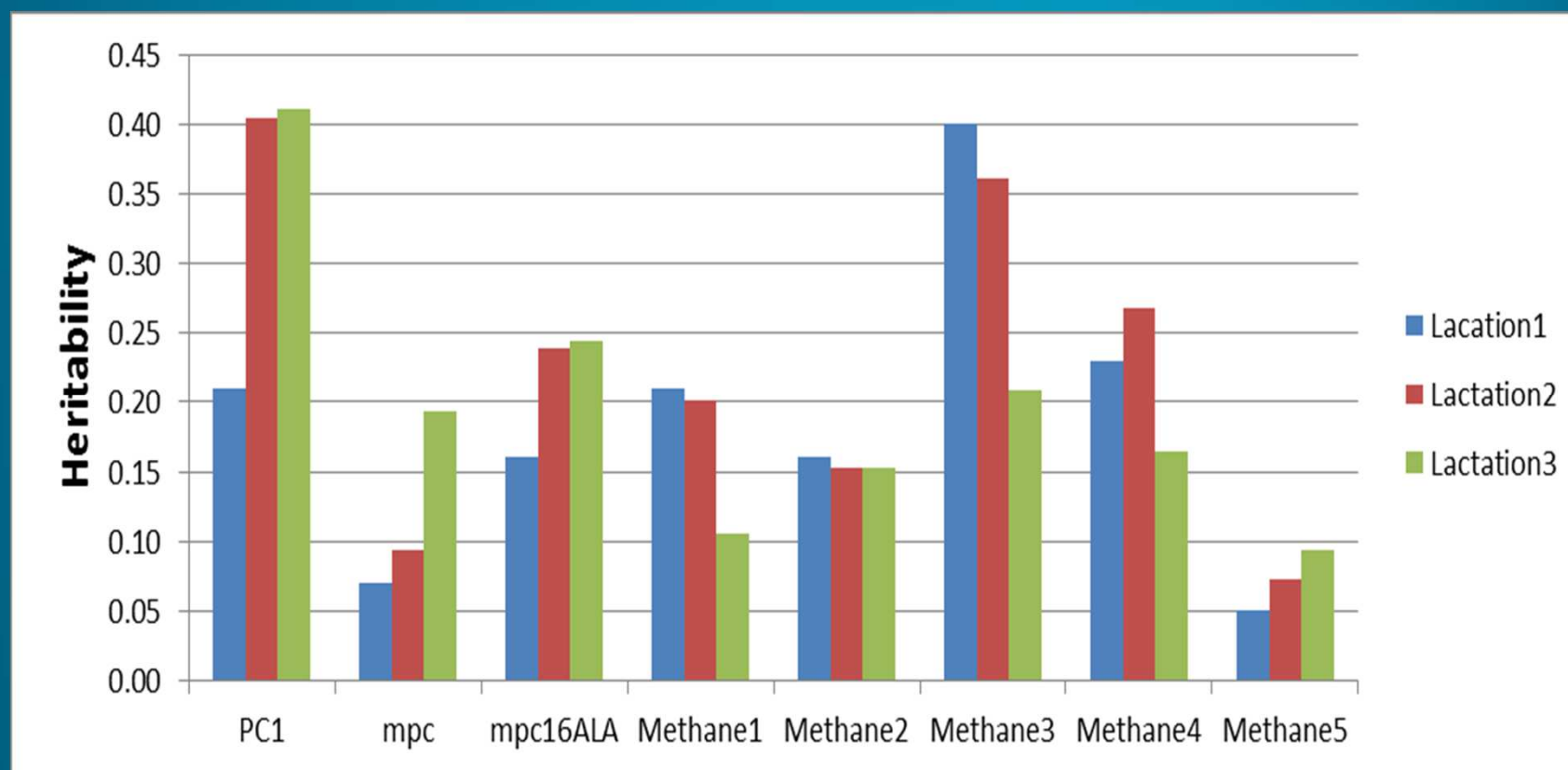
$Q$ : Coefficients of 2<sup>nd</sup> order Legendre polynomials

$X$  and  $Z$ : Incidence matrices

Variance components were calculated by REML

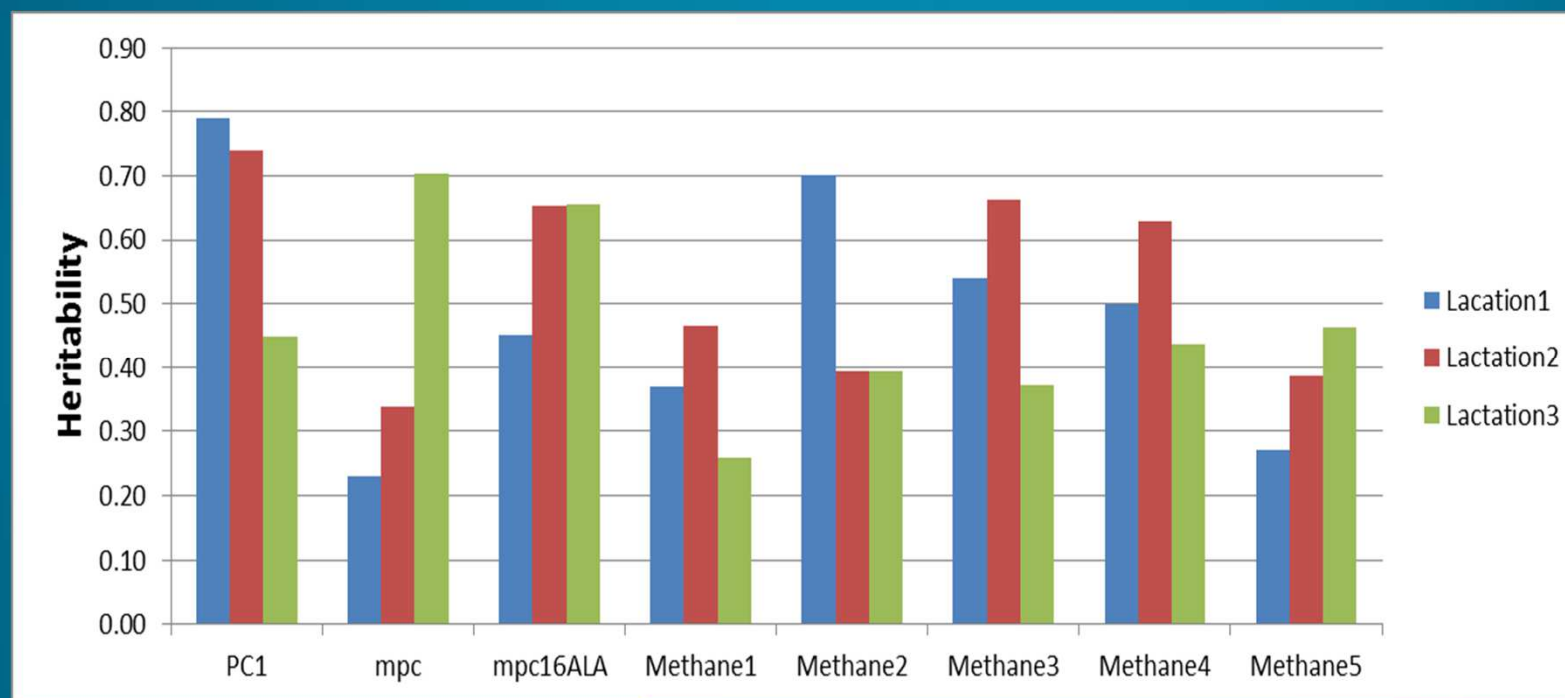
# Heritabilities estimates of indicator traits

## 1. daily heritabilities





## 2. Lactation heritabilities



**Heritability for Predicted Methane Production was 0.12 in Holstein cow (Cassandro et al., 2010)**

Sheep  $0.30 \pm 0.26$   
(respiration chambers)-  
Pinares-Patino et al., 2011;  
0.13 (Robinson et al., 2010)

# Approximate Genetic Correlations

## Lactation 1

Indicator	PC1	PC2	mpc	mpc16ALA	Methane1	Methane2	Methane3	Methane4	Methane5
PC1	1								
PC2	-0.78	1							
mpc	0.07	0.46	1						
mpc16ALA	0.23	0.19	0.54	1					
Methane1	-0.58	0.12	-0.59	-0.55	1				
Methane2	-0.61	0.20	-0.48	-0.51	0.96	1			
Methane3	-0.48	0.26	-0.16	-0.12	0.64	0.70	1		
Methane4	-0.35	-0.03	-0.47	-0.65	0.81	0.71	0.35	1	
Methane5	-0.37	0.10	-0.27	-0.29	0.62	0.61	0.24	0.66	1

Approximate genetic correlations were similar to 2<sup>nd</sup> and 3<sup>rd</sup> Lactation

## Range of EBV for sires which have daughters with CH<sub>4</sub> indicator data

N	Lactation 1 (127 bulls)			Lactation 2 (112 bulls)			Lactation 3 (97 bulls)		
Indicator	SD	Range	Range/SD	SD	Range	Range/SD	SD	Range	Range/SD
PC1	64.09	373.20	5.82	57.89	320.42	5.54	56.00	285.84	5.10
mpc	8.06	52.12	6.47	10.83	66.14	6.11	16.31	82.33	5.05
mpc16ALA	15.67	141.13	9.00	21.92	157.06	7.17	19.06	98.60	5.17
Methane1*	1893	11603	6.13	2027	13019	6.42	1125	6259	5.56
methane2*	1492	9440	6.32	1535	8975	5.85	1091	5932	5.44
Methane3*	3696	21280	5.76	3038	16322	5.37	2082	11180	5.37
Methane4*	2701	13446	4.98	3573	18882	5.28	2174	12208	5.61
methane5^	31.70	226.69	7.15	45.92	270.02	5.88	47.41	277.07	5.84

Methane1-4 g/lactation; methane5 g/kg DM intake

Appreciable genetic difference was observed for e. g. Methane1, 11603 g (11 kg) per lactation

# Range of EBV for Dams which have daughters with CH<sub>4</sub> indicator data

N	Lactation 1 (1301 cows)			Lactation 2 (880 cows)			Lactation 3 (581 cows)		
Indicator	SD	Range	Range/SD	SD	Range	Range/SD	SD	Range	Range/SD
PC1	82.86	544.55	6.57	81.70	510.83	6.25	63.19	402.64	6.37
mpc	7.85	56.32	7.18	10.34	70.29	6.80	17.69	121.74	6.88
mpc16ALA	18.42	139.54	7.57	23.69	156.46	6.60	24.03	144.68	6.02
Methane1*	2179	15133	6.94	2151	13867	6.44	1252	7611	6.08
methane2*	1715	11617	6.77	1628	9630	5.91	1205	6909	5.73
Methane3*	4272	27707	6.48	3641	27304	7.50	2179	13206	6.06
Methane4*	3077	22841	7.42	3525	25368	7.20	2257	14606	6.47
methane5^	34.85	272.85	7.83	45.59	285.16	6.26	55.31	409.39	7.40

Methane1-4 g/lactation; methane5 g/kg DM intake

Appreciable genetic difference was observed for e. g. Methane1, 15113 g (15 kg) per lactation

# Conclusions

- Possible predictions of CH<sub>4</sub> indicators by MIR
- All CH<sub>4</sub> indicators followed the similar pattern.
- The results suggested that there are differences on CH<sub>4</sub> production following the breeds, the lactation numbers and the DIMs
- Preliminary heritability estimates were low to moderate.
- The genetic variability of CH<sub>4</sub> production seems to exist

# Collaborations

- Comité du Lait, Battice, Belgium
- Walloon Breeding Association, Ciney, Belgium
- Walloon Agriculture Research Center, Gembloux
- Teagsac, Ireland
- SAC, Scotland
- Potentially all GHM partners



# PhD Objectives

## 1. Estimate the genetic parameters

1. different breeds
2. different units to express the methane emission
3. Different methodologies (e.g., multiple traits models)

## 2. Develop methane equation

1. Training at Teagasc Moorepark during 4 months
2. Collaboration with a Walloon local project MethaMilk

## 3. Study the relationships between methane production and economic traits currently used in animal selection



# Training and Mobility

Training/Mobility	Date	Institution	ECTS
TEAGSAC, Ireland	02/04/12 - 03/08/12		
Training on infrared spectroscopy and chemometrics	27/02/12 - 02/03/12	CRAW- Belgium	4
Dairy cow lactations, profiles, nutrient allocation and energy balances	05/12/11 - 09/12/11	Aarhus Uni, Denmark	4
Estimation of methane and its variation across different breeds of cattle predicted from milk fatty acids	02/12/11	Paris	
Nutrition and fat metabolism in dairy cattle	17/11/11	Wageningen, the Netherlands	0.3
Training for users of computing devices and mass storage	29/09/11 - 15/12/11	UCL, Belgium	
French Language Course	20/09/11 - 23/02/12	Alpha, Gembloux	

## Priority 1

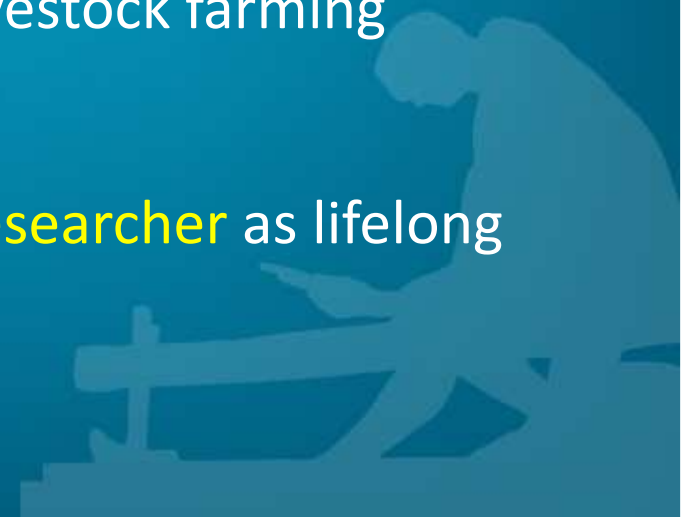
Work in **private industry or breeding associations** to provide consultation to target farmers for reduction of environmental footprint; for example Cadbury, Mars, Nestle or others

## Priority 2

Work in **vulnerable countries** where livestock-environment interactions are not properly looked; where farmer think the emission is natural from beginning of livestock farming

## Priority 3

As all student think, go to **postdoc or researcher** as lifelong obligation



# Acknowledgement



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Thank you for your attention!

